6. (Amended) The method of claim 1, wherein in step III), said tester and normalization and subtraction drivers are mixed together and normalization and subtraction are conducted as a single step.

7. (Amended) The method of claim 1, wherein said normalized and/or subtracted cDNA is long-strand, full-coding, and/or full-length cDNA.

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8. (Amended) The method of claim 1, wherein step III) comprises the addition of an enzyme capable of cleaving single-strand RNA driver nonspecifically bound to single strand cDNA and the cleaved single strand RNA driver is removed.

12. (Amended) The method of claim 1, wherein said cDNA tester is prepared by CAP-trapping the 5′ end of RNA.

13. (Amended) The method of claim 1, wherein the preparation of said cDNA tester comprises the following steps:

(1) synthesizing first strand cDNA by means of reverse transcriptase forming mRNA/cDNA hybrids;

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(2) chemically binding a tag molecule to the diol structure of the 5′ CAP ($^{7Me}G_{ppp}N$) site of mRNA forming hybrids;

(3) trapping long-strand, full-coding, and/or full-length cDNA hybrids; and

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(4) removing single strand mRNA through digestion with an enzyme capable of cleaving single strand mRNA.

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15. (Amended) The method of claim 1, wherein said polynucleotide driver for normalization and/or subtraction is RNA and/or DNA.

17. (Amended) The method of claim 1, wherein said normalization driver comprises cellular mRNA from the same library, the same tissue, or the same cDNA population as what is to be normalized.

18. (Amended) The method of claim 1, wherein said normalization driver comprises single strand cDNA obtained from the same library, the same tissue, or the same cDNA population as what is to be normalized.

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19. (Amended) The method of claim 1, wherein said subtraction driver comprises cellular mRNA from a library, tissue, or cDNA population differing from what is to be subtracted.

20. (Amended) The method of claim 1, wherein said subtraction driver comprises single strand cDNA from a library, tissue, or cDNA population differing from what is to be normalized.

21. (Amended) The method of claim 1, further comprising a step V) of preparing a second strand of recovered cDNA and performing cloning.

26. (Amended) The method of claim 22, wherein said normalized and/or subtracted cDNA is long-strand, full-coding, and/or full-length cDNA.

27. (Amended) The method of claim 22, wherein step III) comprises the addition of an enzyme capable of cleaving single-strand RNA driver nonspecifically bound to single strand cDNA and the cleaved single strand RNA driver is removed.

31. (Amended) The method of claim 22, wherein said cDNA tester is prepared by CAP-trapping the 5' end of RNA.

32. (Amended) The method of claim 22, wherein said normalization driver comprises cellular mRNA from the same library, the same tissue, or the same cDNA population as what is to be normalized.

33. (Amended) The method of claim 22, wherein said normalization driver comprises single strand cDNA obtained from the

same library, the same tissue, or the same cDNA population as what is to be normalized.

34. (Amended) The method of claim 22, wherein said subtraction driver comprises cellular mRNA from a library, tissue, or cDNA population differing from what is to be subtracted.

35. (Amended) The method of claim 22, wherein said subtraction driver comprises single strand cDNA from a library, tissue, or cDNA population differing from what is to be normalized.

36. (Amended) The method of claim 22, further comprising a step V) of preparing a second strand of recovered cDNA and performing cloning.

41. (Amended) The method of claim 37, wherein said normalized and subtracted cDNA is long-strand, full-coding, and/or full-length cDNA.

42. (Amended) The method of claim 37, wherein step III) comprises the addition of an enzyme capable of cleaving single-strand RNA driver nonspecifically bound to single strand cDNA and the cleaved single strand RNA driver is removed.

46. (Amended) The method of claim 37, wherein said cDNA tester is prepared by CAP-trapping 5′ end of RNA.

47. (Amended) The method of claim 37, wherein the preparation of said cDNA tester comprises the following steps:

(1) synthesizing first strand cDNA by means of reverse transcriptase forming mRNA/cDNA hybrids;

(2) chemically binding a tag molecule to the diol structure of the 5′ CAP ($^{7Me}G_{ppp}N$) site of mRNA forming hybrids;

(3) trapping long-strand, full-coding, and/or full-length cDNA hybrids; and

(4) removing single strand mRNA through digestion with an enzyme capable of cleaving single strand mRNA.

49. (Amended) The method of claim 37, wherein said polynucleotide driver for normalization and/or subtraction is RNA and/or DNA.

51. (Amended) The method of claim 37, wherein said normalization driver comprises cellular mRNA from the same library, the same tissue, or the same cDNA population as what is to be normalized.

52. (Amended) The method of claim 37, wherein said normalization driver comprises single strand cDNA obtained from the same library, the same tissue, or the same cDNA population as what is to be normalized.

53. (Amended) The method of claim 37, wherein said subtraction driver comprises cellular mRNA from a library, tissue, or cDNA population differing from what is to be subtracted.

54. (Amended) The method of claim 37, wherein said subtraction driver comprises single strand cDNA from a library, tissue, or cDNA population differing from what is to be normalized.

55. (Amended) The method of claim 37, further comprising a step V) of preparing a second strand of recovered cDNA and performing cloning.

60. (Amended) The method of claim 56, wherein in step c), normalization is conducted first, followed by subtraction.

61. (Amended) The method of claim 56, wherein in step c), subtraction is conducted first, followed by normalization.

62. (Amended) The method of claim 56, wherein in step c), said tester and normalization and subtraction drivers are mixed together and normalization and subtraction are conducted as a single step.

63. (Amended) The method of claim 56, wherein said normalized and/or subtracted cDNA is long-strand, full-coding, and/or full-length cDNA.

64. (Amended) The method of claim 56, wherein the enzyme of said step d) is either selected from the group consisting of RNase I, RNaseA, RNase4, RNaseT1, RNaseT2, RNase2, and RNase3, or comprises a mixture thereof.

65. (Amended) The method of claim 56, wherein the enzyme of said step d) is RNase I.

66. (Amended) The method of claim 56, wherein said cDNA tester is prepared by CAP-trapping the 5' end of RNA.

67. (Amended) The method of claim 56, further comprising the step g) of preparing a second strand of recovered cDNA and performing cloning.

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68. (Amended) The method of claim 1, wherein said tester/driver hybrids are bound to tag molecules.

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70. (Amended) The method of claim 1, wherein said tester/driver hybrids are removed through the use of a matrix.

74. (Amended) The method of claim 72, wherein said antibody covering said beads or said antibody binding said beads is an antiantigen antibody, antibiotin antibody, antiavidin antibody, antistreptavidin antibody, or antidigoxigenin antibody.

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75. (Amended) The method of claim 1, wherein said tester/driver hybrid is removed through the use of streptavidin/phenol.

76. (Amended) The method of claim 1, wherein hydroxyapadite and nonlabeled RNA are employed to remove said tester/driver hybrid.

80. (Amended) The method of claim 77, wherein said RNA/DNA hybrid is a product of normalization.

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81. (Amended) The method of claim 77, wherein said RNA/DNA hybrid is a product of subtraction.

82. (Amended) The method of claim 77, wherein said RNA/DNA hybrid is the product of a method comprising the steps of normalization and subtraction in any order or of a method comprising a single normalization/subtraction step.

85. (Amended) The method of claim 77, wherein said DNA or cDNA is long-chain, full-coding, and/or full-length cDNA.

86. (Amended) The method of claim 1 employed to prepare one, two, or more libraries.

87. (Amended) cDNA or a cDNA library obtainable by the method of claim 1.